Sig. Frame

Init. Opt. Length Score Score

0.85

AAAAAAAAAAAAAATTCAA X

Optimized Score = 142 Significance = 0.85 Matches = 185 Mismatches = 238 Conservative Substitutions = 0

FastDB

```
| 820 | 830 | 840 | 850 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 750 760 770 780 x 790 800
CACCCAGCCTGCATCCCCAGAACCACGAGGGGACATCGCTGTTCCCCCAGAACCCACTATCCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCATAGCCTCAACATTTTGGGAATCTTCCCTTAATCACCCTTGCTCCTCGGGTGCCTGGAAGATGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. US-09-886-241-4 (1-1506)
US-09-886-241-3- Sequence 3, Application US/09886241
                                                             1. US-09-886-241-3- Sequence 3, Application U
2. US-09-886-241-5- Sequence 5, Application U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAGAGACCTCTTTGTTGCGTTTTGTGCT
                                Description
                                                                                                                                                                                                                                                                                                            37
36%
83
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                                                                                                                                                                                                                                                                                                     Initial Score
Residue Identity
                                Sequence Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1170
                                                                                                                                                                                                              Results file 4_x_3_and_5.res made by spaula on Wed 4 Dec 102 14:37:04-PST
                                                                                                                                                                                                                                                                                                                                                                                                                                   Results of the initial comparison of US-09-886-241-4 (1-1505) with:
File : 886241-copy.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Standard Deviation
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                                                                                                                                                                                                                                                                                                            Query sequence being compared:US-09-886-241-4 (1-1506)
Number of sequences searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEARCH STATISTICS

    Fast Pairwise Comparison of Sequences

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33
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2
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- 16
-5
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                                                                                                                                                                                                                                                                                                                                            Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unitary
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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mean
34
> 0 < OI to IntelliGenetics > 0 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Furity matrix
Cap penalty
Gap size penalty
Cap size penalty
Cutoff score
Randomization group
                                                                                                                                                    Release 5.4
```

SCORE 01 STDEV -9

Optimized Score = 647 Significance = -0.57 Matches = 825 Mismatches = 621 Conservative Substitutions = 0 2. US-09-886-241-4 (1-1506) US-09-886-241-5- Sequence 5, Application US/09886241 32 47% 300 Initial Score Residue Identity

A 100% identical sequence to the query sequence was not found.

Times:

The list of best scores is:

1290

1260

1200

1190

4_x_3_and_5.res

Wed

X 10 TAAATTCUCGGCCGCGT-CG TTAAATTCUCGGCCGCGT-CG TTAAATTCUCGGCCGCGT-CG 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 80 80 ACCAGAGAGACTCGAAAAGAAGCCCAAACCAAGGCCCCCAGAGAGGTCCCCCAGGCC	CCTTTG-90 100 110 120 130 140 140 120 130 140 140 140 140 140 140 140 140 140 14	150 160 200 TTCTGAAAAGCTGGA-TCCAGCTTGTTGAAGCCCTTGAGCTGATCTTAGATCC-GGCGCAGG	210 220 280 240 250 260 260 260 AGA	270 320 320 CUTCCCCCACAGAGAGCTCAGGAGAGGGGCACCATCTCA-AGTCGAGAGACCCAACC I I I I I I I I I I I I I I I I

| 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 800 810 820 830 840 850 860 TATCCACCCTGTTTTGTGCTCTCCCCTCG--CCTGCTAGGGCTGCGGCTTCTGACTTCTAGAAGACTAA ---CTTTA--CTCTTAAG-CCTCGAACAATTGAATTTTGAGTCTATGAATACATACATGAGACATCT---1020 1030 1040 1050 1060 a - taggcacc - cagcctgcatctc - ccaggaggaagt - ggaggggacatcgctgttccccagaaacccact

GATCCTCTCCCTGGACACGAGGACCCA-CAGGGCAGGACCCTAAGATCTGGGGAAAGGAGGGT--CCTGAG GGTGATAGATTTTTTACTATTTAGAATAAGGAGTAAAACAATCTTGTCTATTTGTCATCCAGCTCACCAGTT

CACGGAATGCCG------CCTA--GTTTAT---GT-------CCCCGGTGG-------GGCAC